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TI - A genome-wide search for asthma susceptibility loci in ethnically diverse populations

DT - Journal

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AB - Asthma is an inflammatory airways disease assocd. with intermittent respiratory symptoms, bronchial hyper-responsiveness (BHR) and reversible airflow obstruction and is phenotypically heterogeneous. Patterns of clustering and segregation analyses in asthma families have suggested a genetic component to asthma. Previous studies reported linkage of BHR and atopy to chromosomes 5q (refs 7-9), (refs 10-12), 11q (refs 13-15), 14q (ref. 16), and 12q (ref. 17) using candidate gene approaches. However, the relative roles of these genes in the pathogenesis of asthma or atopy are difficult to assess outside of the context of a genome-wide search. One genome-wide search atopic sib pairs has been reported, however, only 12% of their subjects had asthma. We conducted a genome-wide search in 140 families with .gtoreq.2 asthmatic sibs, from three racial groups and report evidence for linkage to six novel regions: 5p15 (P=0.0008) and 17p11.1-q11.2 (P=0.015) in African Americans; 11p15 (P=0.0089) and 19q13 (P=0.0013) in Caucasians; ~~12q33.1~~ (P=0.0005) and 21q21 (P=0.0040) in Hispanics. Evidence for linkage was also detected in five regions previously reported to be linked to asthma -assocd. phenotypes: 5q23-31 (P=0.0187), 6p21.3-23 (P=0.0129), 12q14-24.2 (P=0.0042), 13q21.3-qter (P=0.0014), and 14q11.2-13 (P=0.0062) in Caucasians and 12q14-24.2 (P=0.0260) in Hispanics.